

SEQUENCE LISTING

<110> Bisgard-Frantzen, Henrik
Pedersen, Sven
Svendsen, Allan

<120> Fungamyl-like Alpha-Amylase Variants

<130> 5835.200-US

<140> US 09/710,339

<141> 2000-11-09

<150> US 60/165,786

<151> 1999-11-16

<160> 5

<170> PatentIn version 3.2

<210> 1

<211> 1734

<212> DNA

<213> Aspergillus Oryzae

<220>

<221> CDS

<222> (54)..(1547)

<223> mat_peptide

<220>

<221> mat_peptide

<222> (114)..(1733)

<400> 1

tcacatcaag ctctcccttc tctgaacaat aaacccacaca gaaggcattt atg atg 56
Met
-20

gtc gcg tgg tgg tct cta ttt ctg tac ggc ctt cag gtc gcg gca cct 104
Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala Pro
-15 -10 -5

gct ttg gct gca acg cct gcg gac tgg cga tcg caa tcc att tat ttc 152
Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe
-1 1 5 10

ctt ctc acg gat cga ttt gca agg acg gat ggg tcg acg act gcg act 200
Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr
15 20 25

tgt aat act gcg gat cag aaa tac tgt ggt gga aca tgg cag ggc atc 248
Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile
30 35 40 45

atc gac aag ttg gac tat atc cag gga atg ggc ttc aca gcc atc tgg 296

Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp	
50 55 60	
atc acc ccc gtt aca gcc cag ctg ccc cag acc acc gca tat gga gat	344
Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp	
65 70 75	
gcc tac cat ggc tac tgg cag cag gat ata tac tct ctg aac gaa aac	392
Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn	
80 85 90	
tac ggc act gca gat gac ttg aag gcg ctc tct tcg gcc ctt cat gag	440
Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu	
95 100 105	
agg ggg atg tat ctt atg gtc gat gtg gtt gct aac cat atg ggc tat	488
Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr	
110 115 120 125	
gat gga gcg ggt agc tca gtc gat tac agt gtg ttt aaa ccg ttc agt	536
Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser	
130 135 140	
tcc caa gac tac ttc cac ccg ttc tgt ttc att caa aac tat gaa gat	584
Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp	
145 150 155	
cag act cag gtt gag gat tgc tgg cta gga gat aac act gtc tcc ttg	632
Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu	
160 165 170	
cct gat ctc gat acc acc aag gat gtg gtc aag aat gaa tgg tac gac	680
Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp	
175 180 185	
tgg gtg gga tca ttg gta tcg aac tac tcc att gac ggc ctc cgt atc	728
Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile	
190 195 200 205	
gac aca gta aaa cac gtc cag aag gac ttc tgg ccc ggg tac aac aaa	776
Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys	
210 215 220	
gcc gca ggc gtg tac tgt atc ggc gag gtg ctc gac ggt gat ccg gcc	824
Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala	
225 230 235	
tac act tgt ccc tac cag aac gtc atg gac ggc gta ctg aac tat ccc	872
Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro	
240 245 250	
att tac tat cca ctc ctc aac gcc ttc aag tca acc tcc ggc agc atg	920
Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met	
255 260 265	
gac gac ctc tac aac atg atc aac acc gtc aaa tcc gac tgt cca gac	968
Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp	

270	275	280	285	
tca aca ctc ctg ggc aca ttc gtc gag aac cac gac aac cca cgg ttc				1016
Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg Phe				
	290	295	300	
gct tct tac acc aac gac ata gcc ctc gcc aag aac gtc gca gca ttc				1064
Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe				
	305	310	315	
atc atc ctc aac gac gga atc ccc atc atc tac gcc ggc caa gaa cag				1112
Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln				
	320	325	330	
cac tac gcc ggc gga aac gac ccc gcg aac cgc gaa gca acc tgg ctc				1160
His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu				
	335	340	345	
tcg ggc tac ccg acc gac agc gag ctg tac aag tta att gcc tcc gcg				1208
Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Ala				
	350	355	360	365
aac gca atc cgg aac tat gcc att agc aaa gat acg gga ttc gtg acc				1256
Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr				
	370	375	380	
tac aag aac tgg ccc atc tac aaa gac gac aca acg atc gcc atg cgc				1304
Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg				
	385	390	395	
aag ggc aca gat ggg tcg cag atc gtg act atc ttg tcc aac aag ggt				1352
Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly				
	400	405	410	
gct tcg ggt gat tcg tat acc ctc tcc ttg agt ggt gcg ggt tac aca				1400
Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr				
	415	420	425	
gcc ggc cag caa ttg acg gag gtc att ggc tgc acg acc gtg acg gtt				1448
Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val				
	430	435	440	445
ggt tcg gat gga aat gtg cct gtt cct atg gca ggt ggg cta cct agg				1496
Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg				
	450	455	460	
gta ttg tat ccg act gag aag ttg gca ggt agc aag atc tgt agt agc				1544
Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser				
	465	470	475	
tcg tgaagggtgg agagtatatg atggtactgc tattcaatct ggcattggac				1597
Ser				
agtgagtttg agtttgatgt acagttggag tcgttactgc tgtcatcccc ttatactctt				1657
cgattgtttt tcgaacccta atgccaagca cgctagtcta ttataggaaa aaaaaaaaaa				1717

aaaaaaaaaa aaaaaaa

1734

<210> 2
 <211> 498
 <212> PRT
 <213> Aspergillus Oryzae

<400> 2

Met Val Ala Trp Trp Ser Leu Phe Leu Tyr Gly Leu Gln Val Ala Ala
 -20 -15 -10 -5

Pro Ala Leu Ala Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr
 -1 1 5 10

Phe Leu Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala
 15 20 25

Thr Cys Asn Thr Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly
 30 35 40

Ile Ile Asp Lys Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile
 45 50 55 60

Trp Ile Thr Pro Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly
 65 70 75

Asp Ala Tyr His Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu
 80 85 90

Asn Tyr Gly Thr Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His
 95 100 105

Glu Arg Gly Met Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly
 110 115 120

Tyr Asp Gly Ala Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe
 125 130 135 140

Ser Ser Gln Asp Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu
 145 150 155

Asp Gln Thr Gln Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser
 160 165 170

Leu Pro Asp Leu Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr
175 180 185

Asp Trp Val Gly Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg
190 195 200

Ile Asp Thr Val Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn
205 210 215 220

Lys Ala Ala Gly Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro
225 230 235

Ala Tyr Thr Cys Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr
240 245 250

Pro Ile Tyr Tyr Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser
255 260 265

Met Asp Asp Leu Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro
270 275 280

Asp Ser Thr Leu Leu Gly Thr Phe Val Glu Asn His Asp Asn Pro Arg
285 290 295 300

Phe Ala Ser Tyr Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala
305 310 315

Phe Ile Ile Leu Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu
320 325 330

Gln His Tyr Ala Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp
335 340 345

Leu Ser Gly Tyr Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser
350 355 360

Ala Asn Ala Ile Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val
365 370 375 380

Thr Tyr Lys Asn Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met
385 390 395

Arg Lys Gly Thr Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys
400 405 410

Gly Ala Ser Gly Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr
415 420 425

Thr Ala Gly Gln Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr
430 435 440

Val Gly Ser Asp Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro
445 450 455 460

Arg Val Leu Tyr Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser
465 470 475

Ser Ser

<210> 3
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 3
gaatgacttg gttgacgcgt caccagtcac

30

<210> 4
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 4
atggttcatt tcagaactga cattgagtaa

30

<210> 5
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 5
ttctgtttca tttcgaacta tgaagat

27